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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

MOSSELMAN ET AL.

Serial Number: 08/826,361 Group Art Unit: to be assigned

Filed: March 26, 1997 Examiner: to be assigned

For: NOVEL ESTROGEN RECEPTOR

CLAIM TO PRIORITY UNDER 35 USC 119

Assistant Commissioner of Patents
Washington, D.C. 20231

May 13, 1997

Sir:

The benefit of the filing date of the following prior foreign application is hereby requested for the above-identified application, and the priority provided in 35 USC 119 is hereby claimed:


European Patent Application Nos. 96200820.7, filed March 26, 1996; and 96203284.3, filed November 22, 1996.

In support of this claim, the requisite certified copies of said original foreign applications are filed herewith.

It is requested that the file of this application be marked to indicate that the Applicant has complied with the requirements of 35 USC 119 and that the Patent and Trademark Office kindly acknowledge receipt of this document.

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Respectfully submitted,


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The attached documents are exact copies of the European patent application described on the following page, as originally filed.

Les documents fixés à cette attestation sont conformes à la version initialement déposée de la demande de brevet européen spécifiée à la page suivante.

Patentanmeldung Nr. Patent application No. Demande de brevet n°

96203284.3

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
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Bemerkungen
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Remarques

Novel estrogen receptor

This invention relates to the field of receptors belonging to the superfamily of nuclear hormone receptors, in particular to steroid receptors. The invention relates to DNA encoding a novel steroid receptor, the preparation of said receptor, the receptor protein, and the uses thereof.

Steroid receptors belong to a superfamily of nuclear hormone receptors involved in ligand-dependent transcriptional control of gene expression. In addition, this superfamily consists of receptors for non-steroid hormones such as vitamine D, thyroid hormones and retinoids (Giguère et al, Nature 330, 624-629, 1987; Evans, R.M., Science 240, 889-895, 1988). Moreover, a range of nuclear receptor-like sequences have been identified which encode so-called 'orphan' receptors: these receptors are structurally related to and therefore classified as nuclear receptors, although no putative ligands have been identified yet (B.W. O'Malley, Endocrinology 125, 1119-1170, 1989; D.J. Mangelsdorf and R.M. Evans, Cell, 83, 841-850, 1995).

The superfamily of nuclear hormone receptors share a modular structure in which six distinct structural and functional domains, A to F, are displayed (Evans, Science 240, 889-895, 1988). A nuclear hormone receptor is characterized by a variable N-terminal region (domain A/B), followed by a centrally located, highly conserved DNA-binding domain (hereinafter referred to as DBD; domain C), a variable hinge region (domain D), a conserved ligand-binding domain (hereinafter referred to as LBD; domain E) and a variable C-terminal region (domain F).

The N-terminal region, which is highly variable in size and sequence, is poorly conserved among the different members of

- 2 -

the superfamily. This part of the receptor is involved in the modulation of transcription activation (Bocquel et al, Nucl. Acid Res., 17, 2581-2595, 1989; Tora et al, Cell 59, 477-487, 1989).

5 The DBD consists of approximately 66 to 70 amino acids and is responsible for DNA-binding activity: it targets the receptor to specific DNA sequences called hormone responsive elements (hereinafter referred to as HRE) within the transcription control unit of specific target genes on the
10 chromatin (Martinez and Wahli, In 'Nuclear Hormone Receptors', Acad. Press, 125-153, 1991).

 The LBD is located in the C-terminal part of the receptor and is primarily responsible for ligand binding activity. In this way, the LBD is essential for recognition and binding of
15 the hormone ligand and, in addition possesses a transcription activation function, thereby determining the specificity and selectivity of the hormone response of the receptor. Although moderately conserved in structure, the LBD's are known to vary considerably in homology between the individual members of the
20 nuclear hormone receptor superfamily (Evans, Science 240, 889-895, 1988; P.J. Fuller, FASEB J., 5, 3092-3099, 1991; Mangelsdorf et al, Cell, Vol. 83, 835-839, 1995).

 Functions present in the N-terminal region, LBD and DBD operate independently from each other and it has been shown
25 that these domains can be exchanged between nuclear receptors (Green et al, Nature, Vol. 325, 75-78, 1987). This results in chimeric nuclear receptors, such as described for instance in WO-A-8905355.

30 When a hormone ligand for a nuclear receptor enters the cell by diffusion and is recognized by the LBD, it will bind to the specific receptor protein, thereby initiating an allosteric alteration of the receptor protein. As a result of

- 3 -

this alteration the ligand/receptor complex switches to a transcriptionally active state and as such is able to bind through the presence of the DBD with high affinity to the corresponding HRE on the chromatin DNA (Martinez and Wahli, 'Nuclear Hormone Receptors', 125-153, Acad. Press, 1991). In this way the ligand/receptor complex modulates expression of the specific target genes. The diversity achieved by this family of receptors results from their ability to respond to different ligands.

The steroid receptors are a distinct class of the nuclear receptor superfamily, characterized in that the putative ligands are steroid hormones. The receptors for glucocorticoids (GR), mineralcorticoids (MR), progesterone (PR), androgens (AR) and estrogens (ER) are classical steroid receptors. Furthermore, the steroid receptors have the unique ability upon activation to bind to palindromic DNA sequences, the so called HRE's, as homodimers. The GR, MR, PR and AR recognize the same DNA sequence, while the ER recognizes a different DNA sequence. (Beato et al, Cell, Vol. 83, 851-857, 1995). After binding to DNA, the steroid receptor is thought to interact with components of the basal transcriptional machinery and with sequence-specific transcription factors, thus modulating the expression of specific target genes.

Several HRE's have been identified, which are responsive to the hormone/receptor complex. These HRE's are situated in the transcriptional control units of the various target genes such as mammalian growth hormone genes (responsive to Glucocorticoid, Estrogen, Testosterone), mammalian prolactin genes and progesterone receptor genes (responsive to Estrogen), avian ovalbumin genes (responsive to Progesterone), mammalian methallothionein gene (responsive to Glucocorticoid)

and mammalian hepatic α_{2u} -globulin gene (responsive to Estrogen, Testosterone, Glucocorticoid).

5 The steroid receptors have been known to be involved in embryonic development, adult homeostasis as well as organ physiology. Various diseases and abnormalities have been ascribed to a disturbance in the steroid hormone pathway. Since the steroid receptors exercise their influence as
10 hormone-activated transcriptional modulators, it can be anticipated that mutations and defects in these receptors, as well as overstimulation or blocking of these receptors might be the underlying reason for the altered pattern. A better knowledge of these receptors, their mechanism of action and of
15 the ligands which bind to said receptor might help to create a better insight in the underlying mechanism of the hormone pathway, which eventually will lead to better treatment of the diseases and abnormalities linked to altered hormone/receptor functioning.

20 For this reason cDNA's of the steroid and several other nuclear receptors of several mammals, including humans, have been isolated and the corresponding amino acid sequence have been deduced, such as for example the human steroid receptors PR, ER, GR, MR, and AR, the human non-steroid
25 receptors for vitamine D, thyroid hormones, and retinoids such as retinol A and retinoic acid. In addition, cDNA's well over 100 mammalian orphan receptors have been isolated, for which no putative ligands are known yet (Mangelsdorf et al, Cell, Vol.83, 835-839, 1995). However, there is still a great need
30 for the elucidation of other nuclear receptors, in order to unravel the various roles these receptors play in normal physiology and pathology.

- 5 -

The present invention provides for such a novel nuclear receptor. More specific, the present invention provides for novel steroid receptors, having estrogen mediated activity. Said novel steroid receptors are novel estrogen receptors, which are able to bind and be activated by, for example, estradiol, estrone and estriol.

According to the present invention it has been found that a novel estrogen receptor is expressed as an 8 kb transcript in human thymus, spleen, peripheral blood lymphocytes (PBLs), ovary and testis. Furthermore, additional transcripts have been identified. In testis, an additional transcript of 1.3 kb was detected. Another transcript of approximately 10 kb was identified in ovary, thymus and spleen. These two transcripts are probably generated by alternative splicing of the gene encoding the novel estrogen receptor according to the invention.

Cloning of the cDNA's encoding the novel estrogen receptors according to the invention revealed that several splicing variants of said receptor can be distinguished. At the protein level, these variants differ only at the C-terminal part.

It is true that an estrogen receptor is already known: cDNA encoding the classical ER was isolated (Green, et al, Nature 320, 134-139, 1986; Greene et al, Science 231, 1150-1154, 1986), and its amino acid sequence deduced. Although both ER's share a great deal of homology, the amino acid sequence of both receptors vary considerably. The homology between the classical ER and the novel ER's according to the invention resides predominantly in the DBD's and LBD's of said receptors. Thus, the two receptors are distinct, encoded for by different genes, which belong to the subclass of estrogen receptors.

Furthermore, two orphan receptors, ERR α and ERR β , having an estrogen receptor related structure have been described.

Based on the structural relatedness of $ERR\alpha$ and $ERR\beta$ with the classic ER, these orphans are considered to be members of the estrogen receptor subclass. These receptors, however, have not been reported to be able to bind estrodial or any other hormone that binds to the classic ER, and other ligands which bind to these receptors have not been found yet. The novel estrogen receptor according to the invention distinguishes itself clearly from these receptors since it was found to bind estrogens.

The fact that a novel ER according to the invention has been found is all the more surprising, since any suggestion towards the existence of additional estrogen receptors was absent in the scientific literature: neither the isolation of the classical ER nor the orphan receptors $ERR\alpha$ and $ERR\beta$ suggested or hinted towards the presence of additional estrogen receptors such as the receptors according to the invention. The identification of additional ER's could be a major step forward for the existing clinical therapies, which are based on the presence of one ER and as such ascribe all estrogen mediated abnormalities and/or diseases to this one receptor. The presence of additional estrogen receptors, such as the receptors according to the invention will be useful in the development of hormone analogs that selectively activate either the classic ER or the novel estrogen receptor according to the invention. This should be considered as one of the major advantages of the present invention.

Thus, in one aspect, the present invention provides for isolated cDNA encoding a novel steroid receptor. In particular, the present invention provides for isolated cDNA encoding a novel estrogen receptor.

According to this aspect of the present invention, there is provided an isolated DNA encoding a steroid receptor protein having an N-terminal domain, a DNA-binding domain and a

- 7 -

ligand-binding domain, wherein the amino acid sequence of said DNA-binding domain of said receptor protein exhibits at least 80% homology with the amino acid sequence shown in SEQ ID NO:3, and the amino acid sequence of said ligand-binding domain of said receptor protein exhibits at least 70% homology with the amino acid sequence shown in SEQ ID NO:4.

In particular, the isolated DNA encodes a steroid receptor protein having an N-terminal domain, a DNA-binding domain and a ligand-binding domain, wherein the amino acid sequence of said DNA-binding domain of said receptor protein exhibits at least 90%, preferably 95%, more preferably 98%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:3.

More particularly, the isolated DNA encodes a steroid receptor protein having an N-terminal domain, a DNA-binding domain and a ligand-binding domain, wherein the amino acid sequence of said ligand-binding domain of said receptor protein exhibits at least 75%, preferably 80%, more preferably 90%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:4.

A preferred isolated DNA according to the invention encodes a steroid receptor protein having the amino acid sequence shown in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:21 or SEQ ID NO:25.

A more preferred isolated DNA according to the invention is an isolated DNA comprising a nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:20 or SEQ ID NO:24.

The DNA according to the invention may be obtained from cDNA. Alternatively, the coding sequence might be genomic DNA, or prepared using DNA synthesis techniques.

The DNA according to the invention will be very useful for in vivo expression of the novel receptor proteins according to the invention in sufficient quantities and in substantially pure form.

In another aspect of the invention, there is provided for a steroid receptor comprising the amino acid sequence encoded by the above described DNA molecules.

The steroid receptor according to the invention has an N-terminal domain, a DNA-binding domain and a ligand-binding domain, wherein the amino acid sequence of said DNA-binding domain of said receptor exhibits at least 80% homology with the amino acid sequence shown in SEQ ID NO:3, and the amino acid sequence of said ligand-binding domain of said receptor exhibits at least 70% homology with the amino acid sequence shown in SEQ ID NO:4.

In particular, the steroid receptor according to the invention has an N-terminal domain, a DNA-binding domain and a ligand-binding domain, wherein the amino acid sequence of said DNA-binding domain of said receptor exhibits at least 90%, preferably 95%, more preferably 98%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:3.

More particular, the steroid receptor according to the invention has an N-terminal domain, a DNA-binding domain and a ligand-binding domain, wherein the amino acid sequence of said ligand-binding domain of said receptor exhibits at least 75%, preferably 80%, more preferably 90%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:4.

It will be clear for those skilled in the art that also steroid receptor proteins comprising combined DBD and LBD preferences and DNA encoding such receptors are subject of the invention.

Preferably, the steroid receptor according to the invention comprises an amino acid sequence shown in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:21 or SEQ ID NO:25.

Also within the scope of the present invention are steroid receptor proteins which comprise variations in the amino acid

- 9 -

sequence of the DBD and LBD without loosing their respective DNA-binding or ligand-binding activities. The variations that can occur in those amino acid sequence comprise deletions, substitutions, insertions, inversions or additions of (an) amino acid(s) in said sequence, said variations resulting in amino acid difference(s) in the overall sequence. It is well known in the art of proteins and peptides that these amino acid differences lead to amino acid sequences that are different from, but still homologous with the native amino acid sequence they have been derived from..

Amino acid substitutions that are expected not to essentially alter biological and immunological activities, have been described in for example Dayhof, M.D., Atlas of protein sequence and structure, Nat. Biomed. Res. Found., Washington D.C., 1978, vol. 5, suppl. 3. Amino acid replacements between related amino acids or replacements which have occurred frequently in evolution are, inter alia Ser/Ala, Ser/Gly, Asp/Gly, Asp/Asn, Ile/Val. Based on this information Lipman and Pearson developed a method for rapid and sensitive protein comparison (Science 227, 1435-1441, 1985) and determining the functional similarity between homologous polypeptides.

Variations in amino acid sequence of the DBD according to the invention resulting in an amino acid sequence that has at least 80% homology with the sequence of SEQ ID NO:3 will lead to receptors still having sufficient DNA binding activity. Variations in amino acid sequence of the LBD according to the invention resulting in an amino acid sequence that has at least 70% homology with the sequence of SEQ ID NO:4 will lead to receptors still having sufficient ligand binding activity.

Homology as defined herein is expressed in percentages, determined via PCGENE.

- 10 -

Comparing the amino acid sequence of the classic ER and the ER's according to the invention revealed a high degree of similarity within their respective DBD's. The conservation of the P-box (amino acids E-G-X-X-A) which is responsible for the actual interactions of ER α with the target DNA element (Zilliacus et al., Mol.Endo. 9, 389, 1995; Glass, End.Rev. 15, 391, 1994), is indicative for a recognition of estrogen responsive elements (ERE's) by the ER's according to the invention. Therefore, the classical ER and novel ER's according to the invention may have overlapping target gene specificities. This could indicate that in tissues which co-express both respective ER's, these receptors compete for ERE's. The ER's according to the invention may regulate transcription of target genes differently from classical ER regulation or could simply block classical ER functioning by occupying estrogen responsive elements.

Thus, a preferred steroid receptor according to the invention comprises the amino acid sequence E-G-X-X-A within the P box of the DNA binding domain, wherein X stands for any amino acid. Also within the scope of the invention is isolated DNA encoding such a receptor.

Methods to prepare the receptors according to the invention are well known in the art (Sambrook et al., Molecular Cloning: a Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, latest edition). The most practical approach is to produce these receptors by expression of the DNA encoding the desired protein.

A wide variety of host cell and cloning vehicle combinations may be usefully employed in cloning the nucleic acid sequence coding for the receptor of the invention. For example, useful cloning vehicles may include chromosomal, non-chromosomal and synthetic DNA sequences such as various known

- 11 -

bacterial plasmids and wider host range plasmids and vectors derived from combinations of plasmids and phage or virus DNA. Useful hosts may include bacterial hosts, yeasts and other fungi, plant or animal hosts, such as Chinese Hamster Ovary (CHO) cells or monkey cells and other hosts.

Vehicles for use in expression of the ligand-binding domain of the present invention will further comprise control sequences operably linked to the nucleic acid sequence coding for the ligand-binding domain. Such control sequences generally comprise a promoter sequence and sequences which regulate and/or enhance expression levels. Furthermore an origin of replication and/or a dominant selection marker are often present in such vehicles. Of course control and other sequences can vary depending on the host cell selected.

Techniques for transforming or transfecting host cells are quite known in the art (see, for instance, Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982 and 1989).

Recombinant expression vectors comprising the DNA of the invention as well as cells transformed with said DNA or said expression vector also form part of the present invention.

In a further aspect of the invention, there is provided for a chimeric receptor protein having an N-terminal domain, a DNA-binding domain, and a ligand-binding domain, characterized in that at least one of the domains originates from a receptor protein according to the invention, and at least one of the other domains of said chimeric protein originates from another receptor protein from the nuclear receptor superfamily, provided that the DNA-binding domain and the ligand-binding domain of said chimeric receptor protein originate from different proteins.

- 12 -

In particular, the chimeric receptor according to the invention comprises the LBD according to the invention, said LBD having an amino acid sequence which exhibits at least 70% homology with the amino acid sequence shown in SEQ ID NO:4. In that case the N-terminal domain and DBD should be derived from another nuclear receptor, such as for example PR. In this way a chimeric receptor is constructed which is activated by a ligand of the ER according to the invention and which targets a gene under control of a progesterone responsive element. The chimeric receptors having a LBD according to the invention are useful for the screening of compounds to identify novel ligands or hormone analogs which are able to activate an ER according to the invention.

In addition, chimeric receptors comprising a DBD according to the invention, said DBD having an amino acid sequence exhibiting at least 80% homology with the amino acid sequence shown in SEQ ID NO:3, and a LBD and, optionally, an N-terminal domain derived from another nuclear receptor, can be successfully used to identify novel ligands or hormone analogs for said nuclear receptors. Such chimeric receptors are especially useful for the identification of the respective ligands of orphan receptors.

Since steroid receptors have three domains with different functions, which are more or less independent, it is possible that all three functional domains have been derived from different members of the steroid receptor superfamily.

Molecules which contain parts having a different origin are called chimeric. Such a chimeric receptor comprising the ligand-binding domain and/or the DNA-binding domain of the invention may be produced by chemical linkage, but most preferably the coupling is accomplished at the DNA level with standard molecular biological methods by fusing the nucleic acid sequences encoding the necessary steroid receptor domains. Hence, DNA encoding the chimeric receptor proteins

- 13 -

according to the invention are also subject of the present invention.

Such chimeric proteins can be prepared by transfecting DNA encoding these chimeric receptor proteins to suitable host cells and culturing these cells under suitable conditions.

It is extremely practical if, next to the information for the expression of the steroid receptor, also the host cell is transformed or transfected with a vector which carries the information for a reporter molecule. Such a vector coding for a reporter molecule is characterized by having a promoter sequence containing one or more hormone responsive elements (HRE) functionally linked to an operative reporter gene. Such a HRE is the DNA target of the activated steroid receptor and, as a consequence, it enhances the transcription of the DNA coding for the reporter molecule. In *in vivo* settings of steroid receptors the reporter molecule comprises the cellular response to the stimulation of the ligand. However, it is possible *in vitro* to combine the ligand-binding domain of a receptor to the DNA binding domain and transcription activating domain of other steroid receptors, thereby enabling the use of other HRE and reporter molecule systems. One such a system is established by a HRE presented in the MMTV-LTR (mouse mammary tumor virus long terminal repeat sequence in connection with a reporter molecule like the firefly luciferase gene or the bacterial gene for CAT (chloramphenicol transferase). Other HRE's which can be used are the rat oxytocin promotor, the retinoic acid responsive element, the thyroid hormone responsive element, the estrogen responsive element and also synthetic responsive elements have been described (for instance in Fuller, *ibid.* page 3096). As reporter molecules next to CAT and luciferase β -galactosidase can be used.

Steroid receptors and chimeric receptors according to the present invention can be used for the *in vitro* identification of novel ligands or hormonal analogs. For this purpose binding studies can be performed with cells transformed with DNA according to the invention or an expression vector comprising DNA according to the invention, said cells expressing the steroid receptors or chimeric receptors according to the invention.

The novel steroid receptor and chimeric receptors according to the invention as well as the ligand-binding domain of the invention, can be used in an assay for the identification of functional ligands or hormone analogs for the nuclear receptors.

Thus, the present invention provides for a method for identifying functional ligands for the steroid receptors and chimeric receptors according to the invention, said method comprising the steps of

- a) introducing into a suitable host cell 1) DNA or an expression vector according to the invention, and 2) a suitable reporter gene functionally linked to an operative hormone response element, said HRE being able to be activated by the DNA-binding domain of the receptor protein encoded by said DNA;
- b) bringing the host cell from step a) into contact with potential ligands which will possibly bind to the ligand-binding domain of the receptor protein encoded by said DNA from step a);
- c) monitoring the expression of the receptor protein encoded by said reporter gene of step a).

If expression of the reporter gene is induced with respect to basic expression (without ligand), the functional ligand can be considered as an agonist; if expression of the reporter

- 15 -

gene remains unchanged or is reduced with respect to basic expression, the functional ligand can be a suitable (partial) antagonist.

For performing such kind of investigations host cells which have been transformed or transfected with both a vector encoding a functional steroid receptor and a vector having the information for a hormone responsive element and a connected reporter molecule are cultured in a suitable medium. After addition of a suitable ligand, which will activate the receptor the production of the reporter molecule will be enhanced, which production simply can be determined by assays having a sensitivity for the reporter molecule. See for instance WO-A-8803168. Assays with known steroid receptors have been described (for instance S. Tsai et al., Cell 57, 443, 1989; M. Meyer et al., Cell 57, 433, 1989).

Legends to the figures

Figure 1.

Northern analysis of the novel estrogen receptor. Two different multiple tissue Northern blots (Clontech) were hybridised with a specific probe for the novel estrogen receptor (see examples). Indicated are the human tissues the RNA originated from and the position of the size markers in kilobases (kb).

Figure 2.

Histogram showing the 3- to 4-fold stimulatory effect of 17β -estradiol, estriol and estrone on the luciferase activity mediated by the novel estrogen receptor. An expression vector

- 16 -

encoding the novel estrogen receptor was transiently transfected into CHO cells together with a reporter construct containing the rat oxytocin promoter in front of the firefly luciferase encoding sequence (see examples).

5

Examples

A. Molecular cloning of the novel estrogen receptor.

Two degenerate oligonucleotides containing inosines (I) were based on conserved regions of the DNA-binding domains and the ligand-binding domains of the human steroid hormone receptors.

Primer #1:

5'-GG(GA(C/T)GA(A/G)GC(A/T)TCIGGTG(C/T)CA(C/T)TA(C/T)TA(C/T)GG-3' (SEQ ID NO:7).

Primer #2:

5'-AAGCCTGG(C/G)A(C/T)IC(G/T)(C/T)TTIGCCCAI(C/T)TIAT-3' SEQ ID NO:8).

As template, cDNA from human EBV-stimulated PBLs (peripheral blood leukocytes) was used. One microgram of total RNA was reverse transcribed in a 20 µl reaction containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 4 mM MgCl₂, 1 mM dNTPs (Pharmacia), 100 pmol random hexanucleotides (Pharmacia), 30 Units Rnase inhibitor (Pharmacia) and 200 Units M-MLV Reverse transcriptase (Gibco BRL). Reaction mixtures were incubated at 37°C for 30 minutes and heat-inactivated at 100°C for 5 minutes. The cDNA obtained was used in a 100 µl PCR reaction containing 10 mM Tris-HCl pH 8.3, 50 mM KCl, 1.5 mM MgCl₂, 0.001% gelatin (w/v), 3% DMSO, 1 microgram of primer #1 and primer #2 and 2.5 Units of Amplitaq DNA polymerase (Perkin

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- 17 -

Elmer). PCR reactions were performed in the Perkin Elmer 9600 thermal cycler. The initial denaturation (4 minutes at 94°C) was followed by 36 cycles with the following conditions: 30 sec. 94°C, 30 sec. 45°C, 1 minute 72°C and after 7 minutes at 72°C the reactions were stored at 4°C. Aliquots of these reactions were analysed on a 1.5% agarose gel. Fragments of interest were cut out of the gel, reamplified using identical PCR-conditions and purified using Qiaex II (Qiagen). Fragments were cloned in the PCRII vector and transformed into bacteria using the TA-cloning kit (Invitrogen). Plasmid DNA was isolated for nucleotide sequence analysis using the Qiagen plasmid midi protocol (Qiagen). Nucleotide sequence analysis was performed with the ALF automatic sequencer (Pharmacia) using a T7 DNA sequencing kit (Pharmacia) with vector-specific or fragment-specific primers.

One cloned fragment corresponded to a novel estrogen receptor (ER) which is closely related to the classical estrogen receptor. Part of the cloned novel estrogen receptor fragment (nucleotides 466 to 797 in SEQ ID 1) was amplified by PCR using oligonucleotide #3 TGTTACGAAGTGGGAATGGTGA (SEQ ID NO:9) and oligonucleotide #2 and used as a probe to screen a human testis cDNA library in λ gt11 (Clontech #HL1010b). Recombinant phages were plated (using Y1090 bacteria grown in LB medium supplemented with 0.2% maltose) at a density of 40.000 per 135 mm dish and replica filters (Hybond-N, Amersham) were made as described by the supplier. Filters were prehybridised in a solution containing 0.5 M phosphate buffer (pH 7.5) and 7% SDS at 65°C for at least 30 minutes. DNA probes were purified with Qiaex II (Qiagen), 32P-labeled with a Decaprime kit (Ambion) and added to the prehybridisation solution. Filters were hybridised at 65°C overnight and then washed in 0.5 X SSC/0.1% SDS at 65°C. Two positive plaques were identified and could be shown to be identical. These

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- 18 -

clones were purified by rescreening one more time. A PCR reaction on the phage eluates with the λ gt11-specific primers #4: 5'-TTGACACCAGACCAACTGGTAATG-3' (SEQ ID NO:10) and #5: 5'-GGTGGCGACGACTCCTGGAGCCCG-3' (SEQ ID NO:11) yielded a fragment of 1700 basepairs on both clones. Subsequent PCR reactions using combinations of a gene-specific primer #6: 5'-GTACACTGATTGTAGCTGGAC-3' (SEQ ID NO:12) with the λ gt11 primer #4 and gene-specific primer #7: 5'-CCATGATGATGTCCCTGACC-3' (SEQ ID NO:13) with λ gt11 primer #5 yielded fragments of 450 bp and 1000 bp, respectively, which were cloned in the PCRII vector and used for nucleotide sequence analysis. The conditions for these PCR reactions were as described above except for the primer concentrations (200 ng of each primer) and the annealing temperature (60°C). Since in the cDNA clone the homology with the ER is lost abruptly at a site which corresponds to the exon 7/exon 8 boundary in the ER, it was suggested that this sequence corresponds to intron 7 of the novel ER gene. For verification of the nucleotide sequences of this cDNA clone, a 1200 bp fragment was generated on the cDNA clone with λ gt11 primer #4 with a gene-specific primer #8 corresponding to the 3' end of exon 7: 5'-TCGCATGCCTGACGTGGGAC-3' (SEQ ID NO:14) using the proofreading Pfu polymerase (Stratagene). This fragment was also cloned in the PCRII vector and completely sequenced and was shown to be identical to the sequences obtained earlier.

To obtain nucleotide sequences of the novel ER downstream of exon 7, a degenerate oligonucleotide based on the AF-2 region of the classic ER (#9: 5'-GGC(C/G)TCCAGCATCTCCAG(C/G)A(A/G)CAG-3'; SEQ ID NO:15) was used together with the gene-specific oligonucleotide #10: 5'-GGAAGCTGGCTCACTTGCTG-3' (SEQ ID NO:16) using testis cDNA as template (Marathon ready testis cDNA, Clontech Cat #7414-1). A specific 220 bp fragment corresponding to nucleotides 1112 to

- 19 -

1332 in SEQ ID No. 1 was cloned and sequenced and was shown to contain high homology with the corresponding region in the classic ER. In order to obtain sequences of the novel ER downstream of the AF-2 region, RACE (rapid amplification of cDNA ends) PCR reactions were performed using the Marathon-ready testis cDNA (Clontech) as template. The initial PCR was performed using oligonucleotide #11: 5'-TCTTGTTCTGGACAGGGATG-3' (SEQ ID NO:17) in combination with the AP1 primer provided in the kit. A nested PCR was performed on an aliquot of this reaction using oligonucleotide #10 in combination with the oligo dT primer provided in the kit. Subsequently, an aliquot of this reaction was used in a nested PCR using oligonucleotide #12: 5'-GCATGGAACATCTGCTCAAC-3' (SEQ ID NO:18) in combination with the oligo dT primer. Nucleotide sequence analysis of a specific fragment that was obtained (corresponding to nucleotides 1256 to 1431 in SEQ ID NO 1) revealed a sequence encoding the carboxyterminus of the novel ER ligand-binding domain, including an F-domain and a translational stopcodon.

In order to investigate the possibility that the novel estrogen receptor had additional, upstream translation-initiation codons, RACE-PCR experiments were performed using Marathon-ready testis cDNA (Clontech Cat. # 7414-1). First a PCR was performed using oligonucleotide SEQ ID NO:26 (antisense corresponding to nucleotides 416-396 in SEQ ID NO:1) and AP-1 (provided in the kit). A nested PCR was then performed using oligonucleotide having SEQ ID NO:27 (antisense corresponding to nucleotides 254-241 in SEQ ID NO:1) with AP-2 (provided in the kit). From the smear that was obtained, the region corresponding to fragments larger than 300 basepairs was cut out, purified using the GenecleanII kit (Bio101) and cloned using the TA-cloning kit (Clontech). Colonies were screened by PCR using gene-specific primers (SEQ ID NO:22; and

- 20 -

SEQ ID NO:28, antisense corresponding to nucleotides 124-103 in SEQ ID NO:1). The clone containing the largest insert was sequenced. The nucleotide sequence corresponds to nucleotides 1 to 480 in SEQ ID NO:24. It is clear from this sequence that an in-frame upstream translation initiation codon is present (position 77-79 in SEQ ID NO:24). Upstream of this translational startcodon an in-frame stop-codon is present (11-13 in SEQ ID NO:24). Consequently, the reading frame of the novel estrogen receptor is 530 amino acids, and the receptor has a calculated molecular mass of approximately 59 kD.

To confirm the nucleotide sequences obtained with 5' RACE, human genomic clones were isolated and analysed. A human genomic library in λ EMBL3 (Clontech HL1067J) was screened with a probe corresponding to nucleotides 1 to 416 in SEQ ID NO:1. A strongly hybridizing clone was plaque-purified and DNA was isolated using standard protocols (Sambrook et al, 1989). The DNA was digested with several restriction enzymes, electrophoresed on agarose gel and blotted onto Nylon filters. Hybridisation of the blot with a probe corresponding the above-mentioned RACE fragment (nucleotides 1-480 in SEQ ID NO:24) revealed a hybridizing Sau3A fragment of approximately 800 basepairs. This fragment was cloned into the BamH1 site of pGEM3z and sequenced. The nucleotide sequence was identical to the sequence of the 5'RACE fragments except for one base difference which is probably a PCR-induced point mutation. Nucleotide 172 was a G-residue in the 5'RACE fragment but an A residue in several independent genomic subclones.

B. Identification of two splice variants of the novel estrogen receptor.

Rescreening of the testis cDNA library with a probe corresponding to nucleotides 917 to 1248 in SEQ ID No. 1

- 21 -

yielded two hybridizing clones, the 3' end of which were amplified by PCR (gene-specific primer #8: 5'-GGAAGCTGGCTCACTTGCTG-3' together with primer #4), cloned and sequenced. One clone was shown to contain an alternative exon 8 (exon 8B) of the novel ER. As a consequence of the introduction of this exon through a specific alternative splicing reaction, the reading frame encoding the novel ER is immediately terminated, thereby creating a truncation of the carboxyterminus of the novel ER.

Screening of a human thymus cDNA library (Clontech HL1074a) with the probe corresponding to nucleotides 935 to 1266 in SEQ ID No. 1, revealed another splice variant. The 3' end of one hybridizing clone was amplified using primer #8 with the λ gt10-specific primer #13 5'-AGCAAGTTCAGCCTGTAAAGT-3' (SEQ ID NO:19), cloned in the PCRII vector and sequenced. The obtained nucleotide sequence upstream of the exon 7/exon 8 boundary were identical to the clones identified earlier. However, an alternative exon 8 (exon 8C) was present at the 3' end encoding two C-terminal amino acids followed by a stop-codon.

These two variants of the novel estrogen receptor do not contain the AF-2 region and therefore probably lack the ability to modulate transcription of target genes in a ligand-dependent fashion. However, the variants potentially could interfere with the functioning of the wild-type classic ER and/or the wild-type novel ER, either by heterodimerization or by occupying estrogen response elements. A mutant of the classic ER (ER1-530) has been described which closely resembles the two variants of the novel estrogen receptor described above. ER1-530 has been shown to behave as a dominant-negative receptor i.e. it can block the intracellular activity of the wild type ER (Ince et al, J. Biol. Chem. 268, 14026-14032, 1993).

C. Northern blot analysis.

Human multiple tissue Northern blots (MTN-blots) were purchased from Clontech and prehybridized for at least 1 hour at 65°C in 0.5 M phosphate buffer pH 7.5 with 7% SDS. DNA fragments that were used as probes were 32P-labeled using a labelling kit (Ambion), denatured by boiling and added to the prehybridisation solution. Washing conditions were: 3X SSC at room temperature, followed by 3 X SSC at 65°C, and finally 1 X SSC at 65°C. The filters were then exposed to X-ray films for one week. Two transcripts of approximately 8 kb and 10 kb were detected in thymus, spleen, ovary and testis. In addition, a 1.3 kb transcript is detected in testis.

D. Ligand-dependent transcription activation by the novel estrogen receptor protein.

Cell culture

Chinese Hamster Ovary (CHO K1) cells were obtained from ATCC (CCL61) and maintained at 37°C in a humidified atmosphere (5% CO₂) as a monolayer culture in fetal calf serum-free M505 medium. The latter medium consists of a mixture (1:1) of Dulbecco's Modified Eagle's Medium (DMEM, Gibco 074-200) and Nutrient Medium F12 (Ham's F12, Gibco 074-1700) supplemented with 2.5 mg/ml sodium carbonate (Baker), 55 µg/ml sodium pyruvate (Fluka), 2.3 µg/ml β-mercaptoethanol (Baker), 1.2 µg/ml ethanolamine (Baker), 360 µg/ml L-glutamine (Merck), 0.45 µg/ml sodium selenite (Fluka), 62.5 µg/ml penicillin (Mycopharm), 62.5 µg/ml streptomycin (Serva), and 5% charcoal-treated bovine calf serum (Hyclone).

Recombinant vectors

The novel ER encoding sequence as presented in SEQ ID No 1 was amplified by PCR using oligonucleotides 5'-

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- 23 -

CTTGGATCCATAGCCCTGCTGTGATGAATTACAG-3' (SEQ ID NO:22)

(underlined is the translation initiation codon) and : 5'-

GATGGATCCTCACCTCAGGGCCAGGCGTCACTG-3' (SEQ ID NO:23)

(underlined is the translation stopcodon, antisense). The

5 resulting BamHI fragment (approximately 1450 base pairs) was then cloned in the mammalian cell expression vector pNGV1 behind the SV40 early promoter. In addition, this vector contains the IgG and Muv enhancers.

10 The reporter expression vector was based on the rat oxytocin gene regulatory region (position -363/+16 as a HindIII/ MboI fragment; R.Ivell, and D.Richter, Proc.Natl.Acad.Sci.USA 81, 2006-2010, 1984) linked to the firefly luciferase encoding sequence; the regulatory region of the oxytocin gene were shown to possess functional estrogen
15 hormone response elements in vitro for both the rat (R.Adan, N.Walther, J.Cox, R.Ivell, and P.Burbach, Biochem.Biophys.Res.Comm. 175, 117-122, 1991) and the human (S.Richard, and H.Zingg, J.Biol.Chem. 265, 6098-6103, 1990).

Transient transfection

20 1 x 10⁵ CHO cells were seeded in 6-wells Nunclon tissue culture plates and DNA was introduced by use of lipofectin (Gibco BRL). Hereto, the DNA (1 µg of both receptor and reporter vector in 250 µL Optimem, Gibco BRL) was mixed with an equal volume of lipofectin reagent (7 µL in 250 µL Optimem,
25 Gibco) and allowed to stand at room temperature for 15 min. After washing the cells twice with serum-free medium (M505) new medium (500 µL Optimem, Gibco) was added to the cells followed by the dropwise addition of the DNA-lipofectin mixture. After incubation for a 5 hour period at 37°C cells
30 were washed twice with fenolred-free M505 + 5% charcoal-treated bovine calf serum and incubated overnight at 37°C. After 24 hours hormone (17β-estradiol, etriol or estron) was

- 24 -

added to the medium (100 nmol/L). Cell extracts were made 48 hours posttransfection by the addition of 200 µL lysisbuffer (0.1 M phosphate buffer pH7.8, 0.2% Triton X-100). After incubation for 5 min at 37°C the cell suspension was

5 centrifuged (Eppendorf centrifuge, 5 min) and 20 µL sample was added to 50 µL luciferase assay reagent (Promega). Light emission was measured in a luminometer (Berthold Biolumat) for 10 sec at 562 nm.

Results.

CHO cells transiently transfected with the novel ER expression vector and a reporter plasmid showed a 3 to 4 fold increase in luciferase activity in response to 17-beta-estradiol as compared to untreated cells. A similar transactivation was obtained upon treatment with estriol and

15 estrone. The results indicate not only that the novel ER can bind estrogen hormones but also that the ligand-activated receptor can bind to the ERE within the rat oxytocin promoter and activate transcription of the luciferase reporter gene.

+31 412 650592

- 25 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

- (A) NAME: Akzo nobel n.v.
- (B) STREET: Velperweg 76
- (C) CITY: Arnhem
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 6824 BM
- (G) TELEPHONE: 0412-666379
- (H) TELEFAX: 0412-650592
- (I) TELEX: 37503 akpha nl

10

(ii) TITLE OF INVENTION: Novel estrogen receptor

(iii) NUMBER OF SEQUENCES: 28

20

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

+31 412 650592

- 26 -

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC 60

ACAAGCCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120

5 CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180

GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240

10 GCCAGCCCTG TTA CTGTTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300

GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360

AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420

7 GATAAAACC GCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480

ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA 540

20 AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600

CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG 660

GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC 720

25 ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780

AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTGACC AAGTGCGGCT CTTGGAGAGC 840

30 TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCC GGCAAG 900

CTCATCTTTG CTCCAGATCT TGTTCGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960

CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020

35 CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG 1080

GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG 1140

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- 27 -

ACCGATGCTT TGSTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200
CGCCTGGCTA ACCTCCTGAT GTCCTGTCC CACGTCAGGC ATGCGAGTAA CAAGGGCATG 1260
5 GAACATCTGC TCAACATGAA GTGCAAAAAT GTGGTCCCAG TGTATGACCT GCTGCTGGAG 1320
ATGCTGAATG CCCACGTGCT TCGCGGGTGC AAGTCCTCCA TCACGGGGTC CGAGTGCAGC 1380
CCGGCAGAGG ACAGTAAAAG CAAAGAGGGC TCCCAGAACC CACAGTCTCA GTGA 1434

10

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

25 ATGAATTACA GCATTCCCAG CAATGTCAC T AACTTGAAG GTGGGCCTGG TCGGCAGACC 60
ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120
CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180
30 GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240
GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300
GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360
AAAACAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420
GATAAAAACC GGCACAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480

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- 28 -

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ATGGTGAAST GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA 540
AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600
CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCCTCCTG 660
GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC 720
ATGATGATGT CCGTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780
AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC 840
TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCC GGCAAG 900
CTCATCTTTG CTCCAGATCT TGTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960
CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020
CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG 1080
GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG 1140
ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200
CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTG A 1251

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

+31 412 650592

- 29 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp
 1 5 10 15

Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His
 20 25 30

Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn
 35 40 45

Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val
 50 55 60

Gly Met
 65

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Val Leu Thr Leu Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser
 1 5 10 15

Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr
 20 25 30

Lys Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys Lys
 35 40 45

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- 30 -

Ile Pro Gly Phe Val Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu
50 55 60

5 Glu Ser Cys Trp Met Glu Val Leu Met Met Gly Leu Met Trp Arg Ser
65 70 75 80

Ile Asp His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp
85 90 95

10

Arg Asp Glu Gly Lys Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met
100 105 110

Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys
115 120 125

15

Glu Tyr Leu Cys Val Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr
130 135 140

20

Pro Leu Val Thr Ala Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala
145 150 155 160

His Leu Leu Asn Ala Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys
165 170 175

25

Ser Gly Ile Ser Ser Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu
180 185 190

30

Met Leu Leu Ser His Val Arg His Ala Ser Asn Lys Gly Met Glu His
195 200 205

Leu Leu Asn Met Lys Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu
210 215 220

35

Leu Glu Met Leu Asn Ala His Val Leu
225 230

(2) INFORMATION FOR SEQ ID NO: 5:

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- 31 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro
1 5 10 15

Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp Pro Thr Pro Gly His
20 25 30

Leu Ser Pro Leu Val Val His Arg Gln Leu Ser His Leu Tyr Ala Glu
35 40 45

Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
50 55 60

Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
65 70 75 80

Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
85 90 95

Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
100 105 110

Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
115 120 125

Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
130 135 140

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- 32 -

Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
145 150 155 160

Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
165 170 175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
180 185 190

Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
195 200 205

Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro
210 215 220

Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser
225 230 235 240

Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met
245 250 255

Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Phe
260 265 270

Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met
275 280 285

Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala
290 295 300

Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu Gly Ile
305 310 315 320

Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu
325 330 335

Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met Ile Leu
340 345 350

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- 33 -

Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp Ala Asp
355 360 365

Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp Ala Leu
370 375 380

Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met
385 390 395 400

Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His Ala Ser
405 410 415

Asn Lys Gly Met Glu His Leu Leu Asn Met Lys Cys Lys Asn Val Val
420 425 430

Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn Ala His Val Leu Arg
435 440 445

Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys Ser Pro Ala Glu Asp
450 455 460

Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln Ser Gln
465 470 475

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro

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- 34 -

1 5 10 15
 Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp Pro Thr Pro Gly His
 20 25 30
 5
 Leu Ser Pro Leu Val Val His Arg Gln Leu Ser His Leu Tyr Ala Glu
 35 40 45
 Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
 10 50 55 60
 Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
 65 70 75 80
 15
 Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
 85 90 95
 Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
 100 105 110
 20
 Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
 115 120 125
 Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
 25 130 135 140
 Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
 145 150 155 160
 30
 Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
 165 170 175
 Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
 180 185 190
 35
 Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
 195 200 205
 Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro

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- 35 -

210

215

220

Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser
 225 230 235 240

5

Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met
 245 250 255

10

Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Phe
 260 265 270

Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met
 275 280 285

15

Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala
 290 295 300

Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu Gly Ile
 305 310 315 320

20

Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu
 325 330 335

Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met Ile Leu
 340 345 350

25

Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp Ala Asp
 355 360 365

30

Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp Ala Leu
 370 375 380

Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met
 385 390 395 400

35

Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His Ala Arg
 405 410 415

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- 36 -

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGIGAYGARG CWTGIGGITG YCAYTAYGG

29

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AAGCCTGGS A YICKYTTIG CCAIYTIAT

29

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

+31 412 650592

- 37 -

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTTACGAAG TGGGAATGGT GA

22

10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTGACACCAG ACCAACTGGT AATG

24

25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

+31 412 650592

- 38 -

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 12:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTACACTGAT TTGTAGCTGG AC

22

(2) INFORMATION FOR SEQ ID NO: 13:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCATGATGAT GTCCTGACC

20

35

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

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- 39 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

10 TCGCATGCCT GACGTGGGAC

20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

GGCSTCCAGC ATCTCCAGSA RCAG

24

(2) INFORMATION FOR SEQ ID NO: 16:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

+31 412 650592

- 40 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGAAGCTGGC TCACTTGCTG

20

5 (2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15
}

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTTGTTCTG GACAGGGATG

20

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(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

35 GCATGGAACA TCTGCTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

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- 41 -

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGCAAGTTCA GCCTGTTAAG T

21

(2) INFORMATION FOR SEQ ID NO: 20:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGAAG GTGGGCGCTGG TCGGCAGACC 60

30

ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120

CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180

GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240

35

GCCAGCCCTG TTA CTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300

GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360

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- 42 -

AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420

GATAAAAACC GCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480

5 ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA 540

AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600

CGAGTSCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG 660

10 GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC 720

ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780

AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC 840

TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCCAGCAAG 900

CTCATCTTTG CTCCAGATCT TGTTCCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960

20 CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020

CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG 1080

25 GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACCTGCT GAACGCCGTG 1140

ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200

CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTC TGCCTGA 1257

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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- 43 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

5

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro
 1 5 10 15

10

Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp Pro Thr Pro Gly His
 20 25 30

Leu Ser Pro Leu Val Val His Arg Gln Leu Ser His Leu Tyr Ala Glu
 35 40 45

Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
 50 55 60

Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
 65 70 75 80

20

Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
 85 90 95

25

Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
 100 105 110

Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
 115 120 125

30

Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
 130 135 140

Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
 145 150 155 160

35

Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
 165 170 175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala

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- 44 -

180

185

190

Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
 195 200 205

5

Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro
 210 215 220

10

Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser
 225 230 235 240

Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met
 245 250 255

15

Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Phe
 260 265 270

Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met
 275 280 285

20

Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala
 290 295 300

25

Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu Gly Ile
 305 310 315 320

Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu
 325 330 335

30

Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met Ile Leu
 340 345 350

Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp Ala Asp
 355 360 365

35

Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp Ala Leu
 370 375 380

Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met

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- 45 -

385 390 395 400

Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His Ala Arg

405 410 415

5

Ser Ala

(2) INFORMATION FOR SEQ ID NO: 22:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CTTGGATCCA TAGCCCTGCT GTGATGAATT ACAG

34

25

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GATGGATCCT CACCTCAGGG CCAGGCGTCA CTG

33

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- 46 -

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1898 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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CACGAATCTT TGAGAACATT ATAATGACCT TTGTGCCTCT TCTTGCAAGG TGTTTTCTCA	60
GCTGTTATCT CAAGACATGG ATATAAAAAA CTCACCATCT AGCCTTAATT CTCCTTCCTC	120
CTACAACTGC AGTCAATCCA TCTTACCCCT GGAGCAGGGC TCCATATACA TACCTTCCTC	180
CTATGTAGAC AGCCACCATG AATATCCAGC CATGACATTC TATAGCCCTG CTGTGATGAA	240
TTACAGCATT CCCAGCAATG TCACTAACTT GGAAGGTGGG CCTGGTCGGC AGACCACAAG	300
CCCAAATGTG TTGTGGCCAA CACCTGGGCA CCTTTCCTCT TTAGTGGTCC ATCGCCAGTT	360
ATCACATCTG TATGCGGAAC CTCAAAAGAG TCCCTGGTGT GAAGCAAGAT CGCTAGAACA	420
CACCTTACCT GTAAACAGAG AGACACTGAA AAGGAAGGTT AGTGGGAACC GTTGCGCCAG	480
CCCTGTTACT GGTCCAGGTT CAAAGAGGGA TGCTCACTTC TCGCTGTCT GCAGCGATTA	540
CGCATCGGGA TATCACTATG GAGTCTGGTC GTGTGAAGGA TGTAAGGCCT TTTTAAAAG	600
AAGCATTCAA GGACATAATG ATTATATTTG TCCAGCTACA AATCAGTGTA CAATCGATAA	660
AAACCGGGCG AAGAGCTGCC AGGCCTGCCG ACTTCGGAAG TGTTACGAAG TGGGAATGGT	720

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- 47 -

GAAGTGTGGC TCCCGGAGAG AGAGATGTGG GTACCGCCTT GTGCGGAGAC AGAGAAGTGC 780

CGACGAGCAG CTGCACTGTG CCGGCAAGGC CAAGAGAAGT GGC GGCCACG CGCCCCGAGT 840

5 GCGGGAGCTG CTGCTGGACG CCCTGAGCCC CGAGCAGCTA GTGCTCACCC TCCTGGAGGC 900

TGAGCCGCCC CATGTGCTGA TCAGCCGCCC CAGTGCGCC TTCACCGAGG CCTCCATGAT 960

10 GATGTCCCTG ACCAAGTTGG CCGACAAGGA GTTGGTACAC ATGATCAGCT GGGCCAAGAA 1020

GATTCCCGGC TTTGTGGAGC TCAGCCTGTT CGAUCAAGTG CGGCTCTTGG AGAGCTGTTG 1080

GATGGAGGTG TTAATGATGG GGCTGATGTG GCGCTCAATT GACCACCCCG GCAAGCTCAT 1140

15 CTTTGCTCCA GATCTTGTTT TGGACAGGGA TGAGGGGAAA TGCGTAGAAG GAATTCTGGA 1200

AATCTTTGAC ATGCTCCTGG CAACTACTTC AAGGTTTCGA GAGTTAAAAC TCCAACACAA 1260

20 AGAATATCTC TGTGTCAAGG CCATGATCCT GCTCAATTCC AGTATGTACC CTCTGGTCAC 1320

AGCGACCCAG GATGCTGACA GCAGCCGGAA GCTGGCTCAC TTGCTGAACG CCGTGACCGA 1380

TGCTTTGGTT TGGGTGATTG CCAAGAGCGG CATCTCCTCC CAGCAGCAAT CCATGCGCCT 1440

25 GGCTAACCTC CTGATGCTCC TGTCACAGT CAGGCATGCG AGTAACAAGG GCATGGAACA 1500

TCTGCTCAAC ATGAAGTGCA AAAATGTGGT CCCAGTGTAT GACCTGCTGC TGGAGATGCT 1560

30 GAATGCCCAC GTGCTTCGCG GGTGCAAGTC CTCATCAGG GGTCCGAGT GCAGCCCGGC 1620

AGAGGACAGT AAAAGCAAAG AGGGCTCCCA GAACCCACAG TCTCAGTGAC GCCTGGCCCT 1680

GAGGTGAACT GGGCCACAGA GGTCACAAGC TGAAGCGTGA ACTCCAGTGT GTCAGGAGCC 1740

35 TGGGCTTCAT CTTTCTGCTG TGTGGTCCCT CATTGTTGTA TGGCAGGCTT GGTGATGTAC 1800

CATCCTTCCC TCCACCTTCC CAACTCTCAG GAGTCGGTGT GAGGAAGCCA TAGTTTCCCT 1860

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- 18 -

TGTTAGCAGA GGGACATTTG AATCGAGCGT TTCCACAC

1898

(2) INFORMATION FOR SEQ ID NO: 25:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr
1 5 10 15

Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile
20 25 30

Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe
35 40 45

Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn
50 55 60

Leu Glu Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp
65 70 75 80

Pro Thr Pro Gly His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser
85 90 95

His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser
100 105 110

Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val

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- 49 -

115

120

125

Ser Gly Asn Arg Cys Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg
 130 135 140

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Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His
 145 150 155 160

10

Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
 165 170 175

Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
 180 185 190

15

Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
 195 200 205

Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys
 210 215 220

20

Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His
 225 230 235 240

Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg
 245 250 255

25

Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu
 260 265 270

30

Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
 275 280 285

Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
 290 295 300

35

Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
 305 310 315 320

Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met

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325

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Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly

340

345

350

5

Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys

355

360

365

Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr

10

370

375

390

Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val

385

390

395

400

15

Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala

405

410

415

Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala

420

425

430

20

Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser

435

440

445

Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His

25

450

455

460

Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys

465

470

475

480

30

Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn

485

490

495

Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys

500

505

510

35

Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln

515

520

525

Ser Gln

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- 51 -

530

(2) INFORMATION FOR SEQ ID NO: 26:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTACACTGAT TTGTAGCTGG A

21

(2) INFORMATION FOR SEQ ID NO: 27:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: other nucleic acid
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AGTAACAGGG CTGGCGCAAC GGTTG

25

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:

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- 52 -

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACTGGCGATG GACCACTAAA GG

22

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Claims:

1. Isolated DNA encoding a protein having an N-terminal domain, a DNA-binding domain and a ligand-binding domain,
5 wherein the amino acid sequence of said DNA-binding domain of said protein exhibits at least 80% homology with the amino acid sequence shown in SEQ ID NO:3, and the amino acid sequence of said ligand-binding domain of said protein exhibits at least 70% homology with the
10 amino acid sequence shown in SEQ ID NO:4.
2. Isolated DNA according to claims 1, characterized in that the amino acid sequence of said DNA-binding domain of said protein exhibits at least 90%, preferably 95%, more
15 preferably 98%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:3.
3. Isolated DNA according to claims 1 or 2, characterized in that the amino acid sequence of said ligand-binding domain of said protein exhibits at least 75%, preferably
20 80%, more preferably 90%, most preferably 100% homology with the amino acid sequence shown in SEQ ID NO:4.
4. Isolated DNA according to claims 1 to 3, said DNA encoding a protein comprising the amino acid sequence of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:21 or SEQ ID NO:25.
5. Isolated DNA according to claims 1 to 4, characterized in that said DNA comprises the nucleic acid sequence of SEQ
30 ID NO:1, SEQ ID NO:2, SEQ ID NO:20 or SEQ ID NO:24.
6. A recombinant expression vector comprising the DNA according to any of the claims 1 to 5.

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- 54 -

7. A cell transfected with DNA according to claims 1 to 5 or an expression vector according to claim 6.
8. A cell according to claim 7 which is a stable transfected cell line which expresses the steroid receptor protein according to any of the claims 9 to 11.
9. Protein encoded by DNA according to claims 1 to 5 or an expression vector according to claim 6.
10. Protein according to claim 9, said protein comprising the amino acid sequence of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:21 or SEQ ID NO:25.
11. Chimeric protein having an N-terminal domain, a DNA-binding domain, and a ligand-binding domain, characterized in that at least one of said domains of said chimeric protein originates from a protein according to claims 9 or 10, and at least one of the other domains of said chimeric protein originates from another receptor protein from the nuclear receptor superfamily, provided that the DNA-binding domain and the ligand-binding domain of said chimeric protein originates from different proteins.
12. DNA encoding a protein according to claim 11.
13. Use of a DNA according to claims 1 to 5 or 12, an expression vector according to claim 6, a cell according to claim 7 or 8 or a protein according to claim 9 to 11 in a screening assay for identification of new drugs.

- 55 -

14. A method for identifying functional ligands for the protein according to claims 9 to 11, said method comprising the steps of

- 5 a) introducing into a suitable host cell 1) DNA according to claims 1 to 5 or 12, and 2) a suitable reporter gene functionally linked to an operative hormone response element, said HRE being able to be activated by the DNA-binding domain of the protein encoded by said DNA;
- 10 b) bringing the host cell from step a) into contact with potential ligands which will possibly bind to the ligand-binding domain of the protein encoded by said DNA from step a);
- 15 c) monitoring the expression of the protein encoded by said reporter gene of step a).

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- 56 -

ABSTRACT

The present invention relates to isolated DNA encoding novel estrogen receptors, the proteins encoded by said DNA, chimeric receptors comprising parts of said novel receptors and uses thereof.

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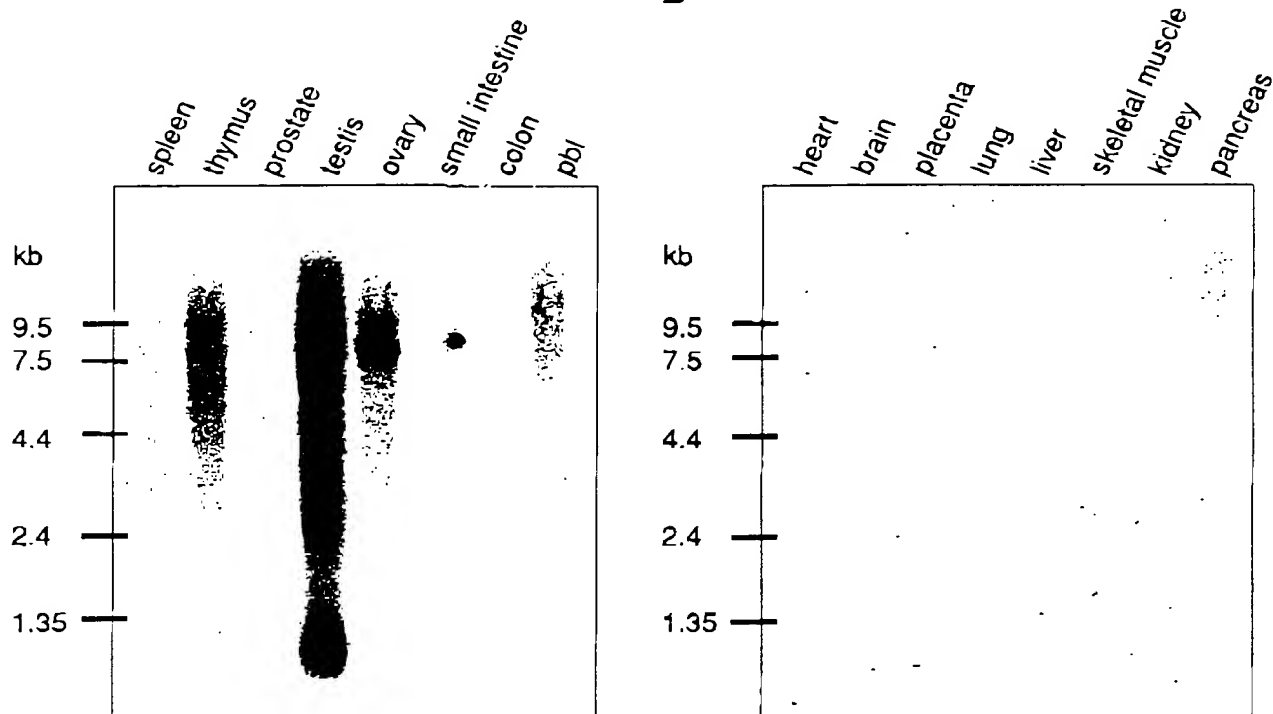


FIG. 1

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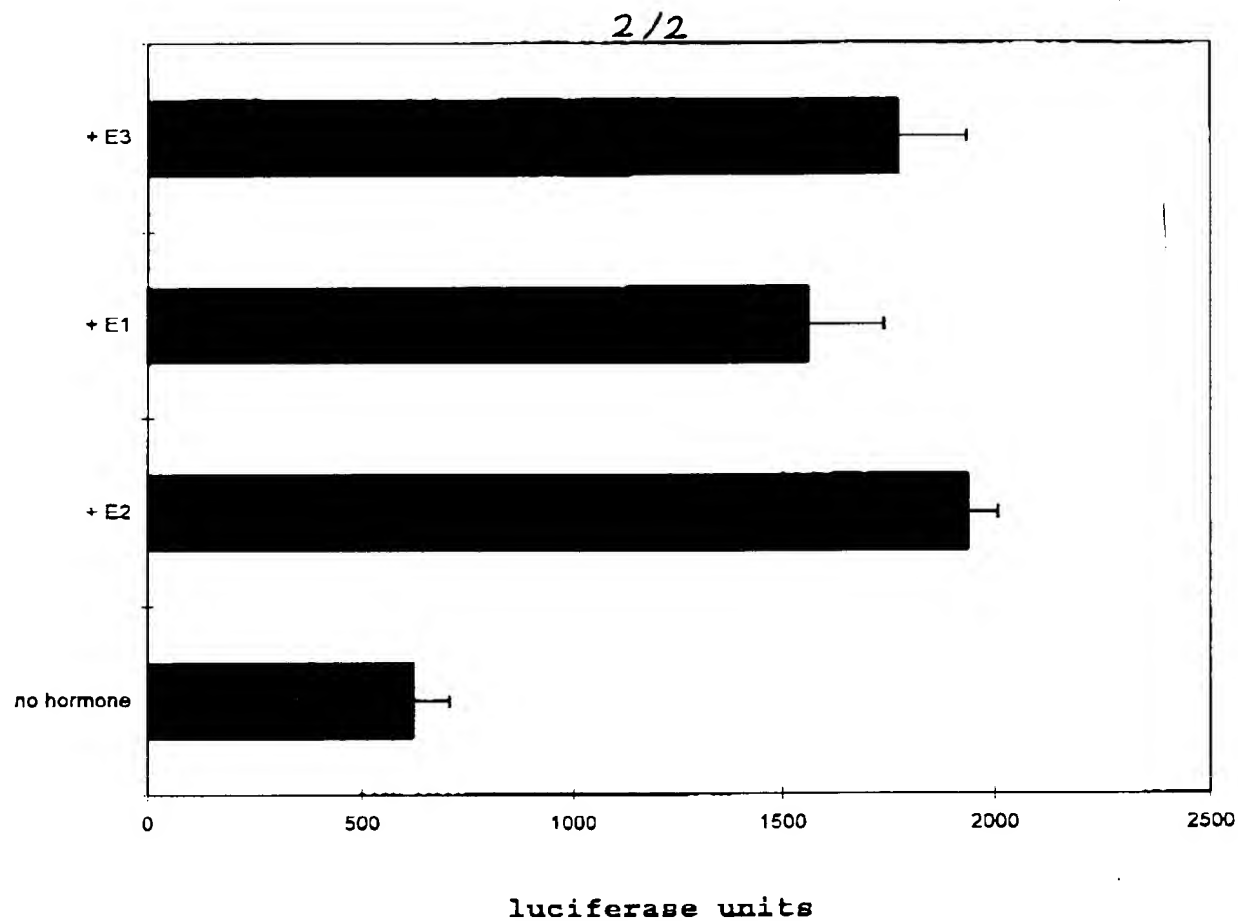


Fig. 2